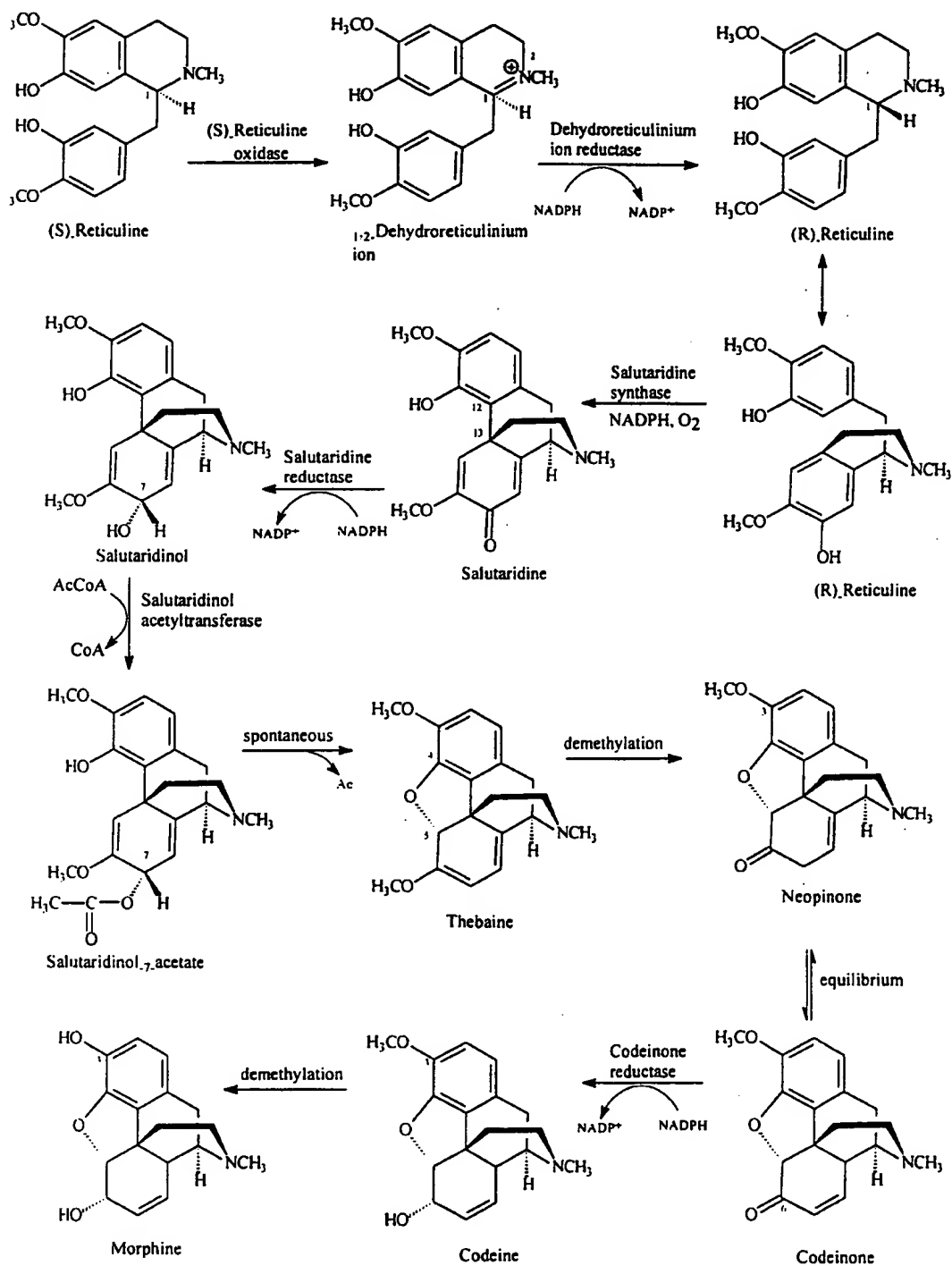


1/11
Fig 1

SCHEME I



2/11

Fig 2

Peptide 3	X L Q E L M A
Peptide 7	V L H Q I A V A R G K
Peptide 14	D D D E L F I T S K
Peptide 16	I P D V V N Q V E M S P T L G Q
Peptide 17	X V N E I P K
Peptide 25	X V A Q V
Peptide 29	I F D N X L T A E D

Fig 3

	51		90
Alfalfa	KQGYRHFDTA	AAYGSEQALG	EALKEAIELG LVTREELFVT
Glycyrrh.	KQGYRHFDTA	AAYGSETALG	EALKEARDLG LVTREELFVT
Soybean	KQGYRHFDTA	AAYGSEQALG	EALKEAIHLG LVSRQDLFVT
Opium poppyELFIT
	91		140
SKLWVTENHP	HLVIPALQKS	LKTLQLDYLD	LYLIHWPLSS QPGKFSFPID
SKLWVTENHP	HLVIPALRKS	LETQLLEYLD	LYLIHWPLSS QPGKFSFPIQ
SKLWVTENHP	HLVLPALRKS	LKTLQLLEYLD	LYLIHWPLSS QPGKFSFPIE
SK.....
	141		190
VADLLPFDVK	GVWESMEESL	KLGLTKAIGV	SNFSVKKLEN LLSVATVLPA
VEDLLPFDVK	GVWESMEECL	KLGLTKAIGV	SNFSVKKLQN LLSVATIRPA
VEDLLPFDVK	GVWESMEECQ	KLGLTKAIGV	SNFSVKKLQN LLSVATIRPV
.....LQE	LMA...IPDV
	191		240
VNQVEMN...	LAWQQKKLRE	FCNANGIVLT	AFSPLRKGAS RGPNEVMEND
VNQVEMN...	LAWQQKKLRE	FCTANGIVLT	AFSPLRKGAS RGPNEVMEND
VDQVEMN...	LAWQQKKLRE	FCKENGIIVT	AFSPLRKGAS RGPNEVMEND
VNQVEMSPTL.....
	241		
MLKEIADAHG	KSVAQISLRW	LYEQGVTFVP	KSVDKERMNQ NLC
MLKGIAEAHG	KSIAQVSLRW	LYEQGVTFVA	KSVDKERMNQ NLQ
VLKEIAEAHG	KSIAQVSLRW	LYEQGVTFVP	KSVDKERMNQ NLH
VLHQIAVARG	K.....VNEIP	K.....

4/11

Fig 4

```

cor1.1 .MESNGVPMI TLSSG...IR MPALGMGTAE TMVKGTEREK LAFLKAIEVG
cor1.2 -----V- --E----- --N-----
cor1.3 -----
cor1.4 -----
6'dcs MAAAEI-T- VFPNSSAQ- --VV---S-P DFTCKKDT.- E-IIE-VKQ-

```

```

cor1.1 YRHFDTAAAY QTEECLEAI AEALQLGLIK SRDELFITSK LWCADAHADL
cor1.2 -----S-----
cor1.3 -----S-----
cor1.4 -----S-----
6'dcs -----GS-QA----L K-IH---VS .-QD-V---- --VTEN-PH-

```

```

cor1.1 VLPALQNSLR NLKLDYLDLY LIHHPVSLKP GKFVNEIPKD HILPMDYKSV
cor1.2 -----E----- --L-----
cor1.3 -----
cor1.4 -----E-----
6'dcs -----RK--K T-Q-E----- --W-L-SQ- ---SFP-EVE DL--F-V-G-

```

```

cor1.1 WAAMEECQTL GFTRAIGVCN FSCKRLQELM ETANSPPVVN QVEMSPTLHQ
cor1.2 -----S----- --K----- A--KI-----
cor1.3 ----- --K----- AA-KI-----
cor1.4 -----S----- --K----- AA-KI-----
6'dcs -ES-----K- -L-K---S- --V-K--N-L SV-TIR---D ----NLAWQ-

```

```

cor1.1 KNLREYCKAN NIMITAHSVL GAVGAAWGTN AVMHKSVLHQ IAVARGKSV
cor1.2 ----- --I--P--S- ---D-----
cor1.3 ----- --IC-P--S- ---D-----
cor1.4 ----- --I--P--S- ---D-----
6'dcs -K---F--E- G-IV--F-P- .RK--SR-P- E--END--KE --E-H---I-

```

```

cor1.1 QVSMRWVYQQ GASLVVKSFN EARMKENLKI FDWELTAEDM EKISEIPQSR
cor1.2 ----- --S-----
cor1.3 ----- -G----- --N-----
cor1.4 ----- -G-----
6'dcs ---L--L-E- -VTF-P--YD KE--NQ--H- ---A--EQ-H H--Q-S--

```

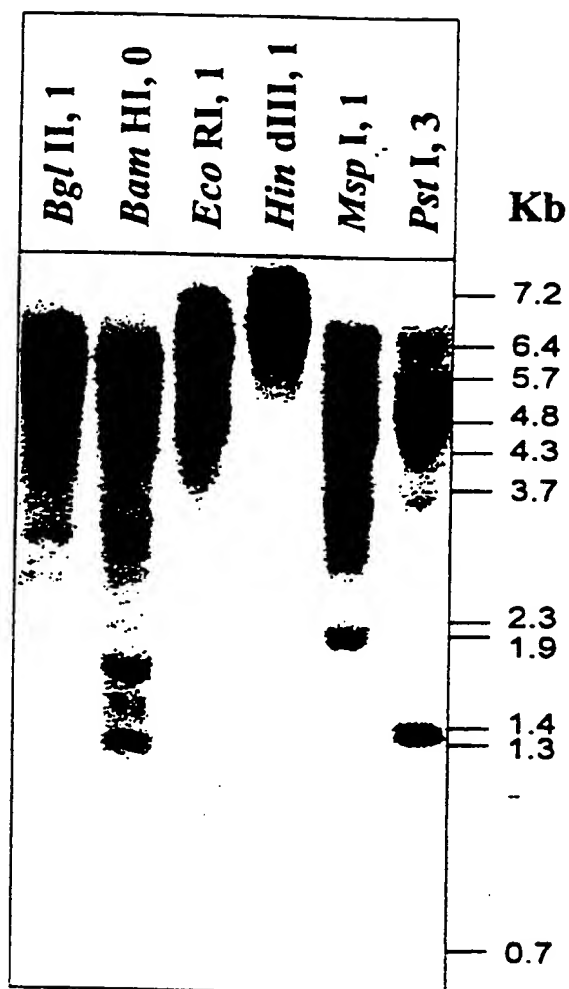
```

cor1.1 TSSAAFLSP TGPFKTEEF WDEKD
cor1.2 ----D-----
cor1.3 ----D-----
cor1.4 -----
6'dcs .....LISG- -K-..QLADL --DQI

```

5/11

FIGURE 5



6/11

FIGURE 6

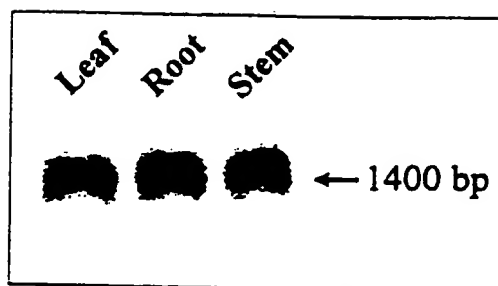
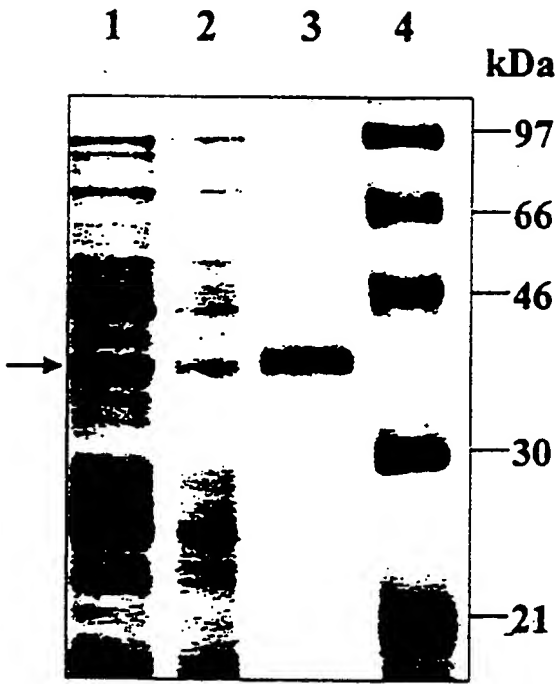
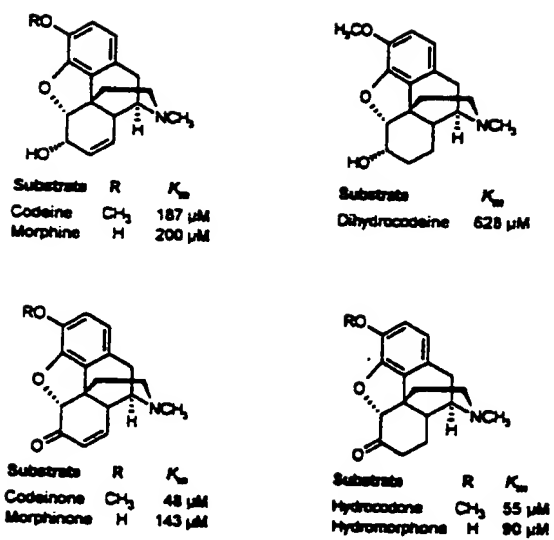


FIGURE 7



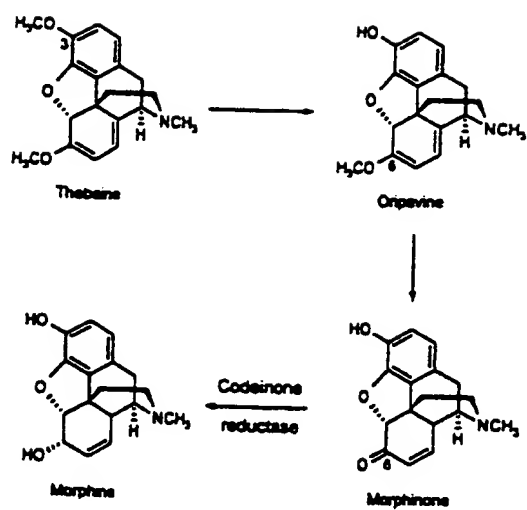
8/11

FIGURE 8



9/11

FIGURE 9



WO 00/58333

PCT/AU00/00249

10/11

cor1.1
cds6-971

Fig 10

GAAAAATGGAGAGTAATGGTGTACCTATGATCACTCTCAGTTCCGGCATTCCGGATGCCTGCTTTAGGTATGGGAA
CAGCTGAAACAATGGTAAAAGGAACAGAAAGAGAGAAATTGGCGTTTTTGAAGCGATAGAGGTCGGTTACAGAC
ACTTCGATACAGCTGCTGCATACCAAAGTGAAGAGTGTCTTGGTGAAGCTATAGCTGAAGCACTTCAACTTGGTC
TAATAAAATCTCGAGATGAACCTTTCATCACTTCCAAGCTCTGGTGCGCTGATGCTCAGCTGATCTTGTCTCTCC
CTGCTCTTCAGAATTCTCTGAGGAATCTTAAATTGGACTATCTTGATCTATATTTGATACACCATCCGGTAAGCT
TGAAGCCAGGGAAGTTTGTAAACGAAATACCAAAGGATCATATCCTTCCAATGGACTACAAATCTGTATGGGCAG
CCATGGAAGAGTGTGAGACCCTTGGCTTCACTAGGGCAATCGGGGTCTGTAATTTCTCATGCAAAAAGGCTTCAAG
AGTTGATGGAAACAGCCAACAGCCCTCCAGTTGTGAATCAAGTGGAGATGAGCCCGACTTTACATCAAAAAAATC
TGAGGGAATATTGCAAGGCCAATAATATCATGATCACCACACTCAGTTTGGGAGCCGTAGGTGCCGCTGGG
GCACCAATGCAGTTATGCATTCTAAGGTGCTTACCAGATTGCTGTGGCCAGAGGAAAATCTGTTGCCAGGTTA
GTATGAGATGGGTTTACCAGCAAGGCGCGAGTCTTGTGGTGAAAAGTTTCAATGAAGCGAGGATGAAGGAAAACC
TTAGATATTTGATTGGGAACCTAACGGCAGAAGACATGGAAAAGATCAGTGAGATTCCACAACTAGAACAAAGCT
CTGCTGCTTTCTTGTATTACCCGACTGGACCTTTCAAACTGAAGAAGAGTTCTGGGATGAGAAGGATTGAACA
TCAATTATAGATGGTAAGTGAGGACTGTCAAAAAGTAATCAGTTTTTCCCTCCGTTTTG

cor1.2
cds 1-966

Fig 11

ATGGAGAGTAATGGTGTACCTATGATCACTCTCAGTTCCGGCATTCCGGATGCCTGCTTTAGGTATGGGAACAGTT
GAAACAATGGAAAAGGGAACAGAAAGAGAGAAATTGGCGTTTTTGAATGCGATAGAGGTCGGTTACAGACACTTC
GATACAGCTGCTGCATACCAAAGTGAAGAGTGTCTTGGTGAAGCTATAGCTGAAGCACTTCAACTTGGTTAATA
AAATCTCGAGATGAACCTTTCATCACTTCCAAGCTCTGGTGCGCTGATGCTCAGCTGATCTTGTCTCTCCCTGCT
CTTCAGAATTCTCTGAGGAATCTCAAATTGGAGTACCTTGATCTATATTTGATACACCATCCGGTAAGCTTGAAG
CCAGGGAAGCTTGTAAACGAAATACCAAAGGATCATATCTTCCAATGGACTACAAATCTGTATGGGCAGCCATG
GAAGAGTGTGAGACCCTTGGCTTCACTAGGGCAATCGGTGTGAGTAATTTCTCATGCAAAAAGCTTCAAGAGTTG
ATGGCAACAGCCAAGATCCCTCCAGTTGTGAATCAAGTGGAGATGAGCCCGACTTTACATCAAAAAAATCTGAGG
GAATATTGCAAGGCCAATAATATCATGATCACTGCACACTCGGTTTTGGGAGCCATAGGTGCTCCATGGGGCAGC
AACGCAGTTATGGATTCTAAGGTGCTTACCAGATTGCTGTGGCAAGAGGAAAATCTGTTGCCAGGTTAGTATG
AGATGGGTTTACCAGCAAGGCGCGAGTCTTGTGGTGAAAAGTTTCAATGAAGCGAGGATGAAGGAAAACCTTAAG
ATATTTGATTCCGAACTAACGGCAGAAGATATGGAAAAGATCAGTGAGATTCCGCAATCTAGAACAAAGCTCTGCT
GATTTCTTGTATCACCAGCTGGACCTTTCAAACTGAAGAAGAGTTCTGGGATGAGAAGGATTGA

cor1.3
cds1-966

Fig 12

ATGGAGAGTAATGGTGTACCTATGATCACTCTCAGTTCCGGCATTCCGGATGCCTGCTTTAGGTATGGGAACAGCT
GAAACAATGGTAAAAGGAACAGAAAGAGAGAAATTGGCGTTTTTGAAGCGATAGAGGTCGGTTACAGACACTTC
GATACAGCTGCTGCATACCAAAGTGAAGAGTGTCTTGGTGAAGCTATAGCTGAAGCACTTCAACTTGGTCTAATA
AAATCTCGAGATGAACCTTTCATCACTTCCAAGCTCTGGTGCGCTGATGCTCAGCTGATCTTGTCTCTCCCTGCT
CTTCAGAATTCTCTGAGGAATCTTAAATTGGACTATCTTGATCTATATTTGATACACCATCCGGTAAGCTTGAAG
CCAGGGAAGTTTGTAAACGAAATACCAAAGGATCATATCCTTCCAATGGACTACAAATCTGTATGGGCAGCCATG
GAAGAGTGTGAGACCCTTGGCTTCACTAGGGCAATCGGGGTCTGTAATTTCTCATGCAAAAAGCTTCAAGAGTTG
ATGGCAGCAGCCAAGATCCCTCCAGTTGTGAATCAAGTGGAGATGAGCCCGACTTTACATCAAAAAAATCTGAGG
GAATATTGCAAGGCCAATAATATCATGATCACTGCACACTCGGTTTTGGGAGCCATAGGTGCTCCATGGGGCAGC
AATGCAGTTATGGATTCTAAGGTGCTTACCAGATTGCTGTGGCAAGAGGAAAATCTGTTGCCAGGTTAGTATG
AGATGGGTTTACCAGCAAGGCGCGAGTCTAGTGGTGAAAAGTTTCAATGAAGGGAGGATGAAGGAAAACCTTAAG
ATATTTGATTGGGAACCTAACGGCAGAGAATATGGAAAAGATCAGTGAGATTCCGCAATCTAGAACAAAGCTCTGCT
GATTTCTTGTATCACCAGCTGGACCTTTCAAACTGAAGAAGAGTTCTGGGATGAGAAGGATTGA

cor1.4
cds1-966

Fig 13

ATGGAGAGTAATGGTGTACCTATGATCACTCTCAGTTCCGGCATTCCGGATGCCTGCTTTAGGTATGGGAACAGCT
GAAACAATGGTAAAAGGAACAGAAAGAGAGAAATTGGCGTTTTTGAAGCGATAGAGGTCGGTTACAGACACTTC
GATACAGCTGCTGCATACCAAAGTGAAGAGTGTCTTGGTGAAGCTATAGCTGAAGCACTTCAACTTGGTTAATA
AAATCTCGAGATGAACCTTTCATCACTTCCAAGCTCTGGTGCGCTGATGCTCAGCTGATCTTGTCTCTCCCTGCT

WO 00/58333

PCT/AU00/00249

11/11

CTTCAGAAATTCCTGAGGAATCTCAAATTGGAGTATCTTGATCTATATTTGATACACCATCCGGTAAGCTTGAAG
CCAGGGAAATTTGTTAACGAAATACCAAAGGATCATATTCTTCCAATGGACTACAAATCTGTATGGGCAGCCATG
GAAGAGTGTGAGACCCTTGGCTTCACTAGGGCAATCGGTGTCAGTAATTTCTCATGCAAAAAGCTTCAAGAGTTG
ATGGCAGCAGCCAAGATCCCTCCAGTTGTGAATCAAGTGGAGATGAGCCCTACTTTACATCAAAAAAATCTGAGG
GAATATTGCAAGGCCAATAATATCATGATCACTGCACACTCGGTTTTGGGAGCCATAGGTGCTCCATGGGGCAGC
AATGCAGTTATGGATTCTAAGGTGCTTACCAGATTGCTGTGGCAAGAGGAAAAATCTGTTGCCAGGTTAGTATG
AGATGGGTTTACCAGCAAGGCGCGAGTCTTGTGGTGAAGTTTCAATGAAGGGAGGATGAAGGAAAACCTTAAG
ATATTTGATTGGGAACTAACGGCAGAAGATATGGAAAAGATCAGTGAGATTCCGCAATCTAGAACAAGCTCTGCT
GCTTTCTTGTTATCACCAGTGGACCTTCAAACCTGAAGAAGAGTTCTGGGATGAGAAGGATTGA

cor1.5
partial seq

Fig 14

TGTGGTGAATCAGGTGGAGATGTGGCCGACTTTACATCAAAAAAATCTGAGGGAATATTGCAAGGCCAATAATAT
CATGATCACTGCACACTCGGTTTTGGGAGCCATAGGTGCTCCATGGGGCAGCAATGCAGTTATGGATTCTAAGGT
GCTT

cor1.6
partial seq

Fig 15

CTCTGGTGCGCTGATGCTCACGCTGATCTTGTCTCCCTGCTCTTCAGAAATTCCTGAGGAATCTCAAATTGGAC
TACCTTGATCTATATTTGATACACCATCCGGTAAGCTTGAAGCCAGGGAAGCTTGTTAACGAAATACCAAAGGAT
CATATTCTTCCAATGGACTACAAATCTGTATGGGCAGCCATGGAAGAGTGTGAGACCCTTGGCTTCACTAGGGCA
ATCGGTGTCAGTAATTTCTCATGCAAAAAGCTTCAAGAGTTGATGGCAACAGCCAAGATCCCTCCA